

GenCore version 5.1.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 13:26:41 ; Search time 190 Seconds
(without alignments)
2594.647 Million cell updates/sec

Title: US-10-602-441-4
Perfect score: 5901
Sequence: 1 MTRAPRCPAVRSLLRSRYRE.....TILKAADPALSTDFQTILD 1122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5901	100.0	1122	2	AAY26579 Murine te
2	5901	100.0	1122	8	ADG90601 Murine TE
3	5954	99.2	1122	5	ABR06711 Mouse tel
4	4859	82.3	1122	8	ADG90609 TERT cons
5	4751	80.5	1128	7	Add21416 Golden ha
6	4751	80.5	1128	8	ADG90603 Hamster T
7	3505	59.4	1132	2	AAY46957 Human tel
8	3505	59.4	1132	2	AAY90251 Human cat
9	3505	59.4	1132	2	AAY28881 Human tel
10	3505	59.4	1132	2	AAY32090 Human tel
11	3505	59.4	1132	2	AAY43621 A human t
12	3505	59.4	1132	2	AAY26580 Human tel
13	3505	59.4	1132	4	AAG64859 Heart mus
14	3505	59.4	1132	4	AAG64329 Human pro
15	3505	59.4	1132	4	AAB99930 Human tel
16	3505	59.4	1132	4	AAB82765 Human tel
17	3505	59.4	1132	5	AAB29226 Human tel
18	3505	59.4	1132	5	AAY72735 Human tel
19	3505	59.4	1132	6	ABR42384 Human tel
20	3505	59.4	1132	6	ABR42063 Human tel
21	3505	59.4	1132	6	ABP56676 Human tel
22	3505	59.4	1132	6	ABR58045 Human tel
23	3505	59.4	1132	7	Add21420 Human TER
24	3505	59.4	1132	7	ADH72743 Human pro

25	3505	59.4	1132	8	ADG70114	Adg70114 hTERT pro
26	3505	59.4	1132	8	ADG90599	Adg90599 Human TER
27	3505	59.4	1132	8	ADI82172	Adi82172 Human tel
28	3505	59.4	1132	8	ADR70482	Adr70482 Human tel
29	3505	59.4	1132	9	ADY25759	Ady25759 Human tel
30	3505	59.4	1154	2	AAW61350	AAW61350 Human tel
31	3505	59.4	1189	2	AAW47008	AAW47008 Glutathio
32	3499	59.3	1285	2	AAW47000	AAW47000 HIS tagge
33	3498	59.3	1132	2	AAW71376	AAW71376 Human tel
34	3498	59.3	1132	2	AAY00627	Aay00627 Human tel
35	3498	59.3	1132	2	AAY00638	Aay00638 Truncated
36	3498	59.3	1132	2	AAY28401	Aay28401 Human EST
37	3498	59.3	1132	3	AAY96566	Aay96566 hEST2, a
38	3498	59.3	1132	7	ADC47061	Adc47061 Human TER
39	3498	59.3	1132	7	ADA40482	Ada40482 Human tel
40	3498	59.3	1132	9	AEA38666	Aea38666 Human tel
41	3496	59.2	1132	2	AAW56113	AAW56113 Human tel
42	3486.5	59.1	1199	2	AAW47007	AAW47007 Glutathio
43	3471	58.8	1166	2	AAY00647	Aay00647 Telomeras
44	3463	58.7	1405	2	AAW56101	AAW56101 Enhanced
45	3435	58.2	1120	2	AAY00641	Aay00641 Telomeras

ALIGNMENTS

RESULT 1
AAY26579
ID AAY26579 standard; protein; 1122 AA.
XX AC AAY26579;
XX 13-SEP-1999 (first entry)
XX DE Murine telomerase reverse transcriptase (mTERT) enzyme.
XX KW Telomerase reverse transcriptase; TERT; mouse; telomere length assay;
KW immunogen; enzyme; telomerase-mediated DNA replication.
XX OS Mus sp.
XX PN WO9927113-A1.
XX PD 03-JUN-1999.
XX PF 25-NOV-1998; 98MO-US025211.
XX PR 26-NOV-1997; 97US-00979742.
PR 16-MAR-1998; 98US-00042460.
XX (GERO-) GERON CORP.
XX (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
XX PI Morin GB, Allsopp R, Depinho R, Greenberg R;
XX WPI; 1999-347722/29.
XX N-PSDB; AAX80994.
XX PT Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and
XX nucleic acids.
XX Claim 8; Fig 2; 135pp; English.
XX The invention relates to a mouse telomerase reverse transcriptase (mTERT)
XX enzyme. Compositions containing mTERT can be used in telomere length
XX assays. Isolated mTERT is useful as an immunogen for the production of
XX monoclonal or polyclonal antibodies. The method is useful for assessing
XX the degree of purification and identification of new mTERT species, such
XX as an mTERT allele, homolog or isoform, or to screen for modulators
XX (antagonists and agonists) of telomerase-mediated DNA replication.
XX Antagonists and agonists of mTERT can be used to modify the activity of
XX other telomerase enzymes such as human TERT (hTERT). The present sequence
XX represents a mTERT enzyme

XX	SQ	Sequence 1122 AA;																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
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Db 121 SYLNTVETLRVSGAWMLLSRVGDDLLVYLAHCALYLLPVPSCAYQVCGSPLYQICA 180
Qy 181 TTDIWPVSASVYRTPRPGVGRNTNLRFLQOIKSSSRQEAPEKPLALPSRGTKRHLSLTSTS 240
Db 181 TTDIWPVSASVYRTPRPGVGRNTNLRFLQOIKSSSRQEAPEKPLALPSRGTKRHLSLTSTS 240
Qy 241 VPSAKKARCYPPRVVEEGPHRQVLPTPSGKSWPSPARSPVPTAEKOLSSKGKVDLSL 300
Db 241 VPSAKKARCYPPRVVEEGPHRQVLPTPSGKSWPSPARSPVPTAEKOLSSKGKVDLSL 300
Qy 301 SGSVCKKHKPSSTLSLSPRONAFQLRPFETRHFLYSRGDQERLNPFLSNLPNLT 360
Db 301 SGSVCKKHKPSSTLSLSPRONAFQLRPFETRHFLYSRGDQERLNPFLSNLPNLT 360
Qy 361 GARRLVEIIFLGSRRPRTSGPLCRTHLSRRYQWMPPLFOQLLVNHAECQYVRLLSHCRF 420
Db 361 GARRLVEIIFLGSRRPRTSGPLCRTHLSRRYQWMPPLFOQLLVNHAECQYVRLLSHCRF 420
Qy 421 RTANQOQVTDALNTSPHMLDLRLHSSPMQVYGFRLACLCCKVVSASLWGTNRNRRFPKN 480
Db 421 RTANQOQVTDALNTSPHMLDLRLHSSPMQVYGFRLACLCCKVVSASLWGTNRNRRFPKN 480
Qy 481 LKPFISLGKYGKLSQELMWKQVEDCHWLRSRPGKDRVPAAEHRLRERILATFLFWLMD 540
Db 481 LKPFISLGKYGKLSQELMWKQVEDCHWLRSRPGKDRVPAAEHRLRERILATFLFWLMD 540
Qy 541 TVVQQLLSFFYITESTFOKNLFFVRKSVWKLQSIGVROHLRVRLRELQOEVRHQ 600
Db 541 TVVQQLLSFFYITESTFOKNLFFVRKSVWKLQSIGVROHLRVRLRELQOEVRHQ 600
Qy 601 DTWLAMPICRLRFIPKPNGLRPIVNMYSMGTRALGRKQAQHFQRLKTLFSLMYERT 660
Db 601 DTWLAMPICRLRFIPKPNGLRPIVNMYSMGTRALGRKQAQHFQRLKTLFSLMYERT 660
Qy 661 KHPHLMGSSVLGMNDIYRTWRAFVLRLALDOTPRMYFKADVTGAYDAIPQKLVVVA 720
Db 661 KHPHLMGSSVLGMNDIYRTWRAFVLRLALDOTPRMYFKADVTGAYDAIPQKLVVVA 720
Qy 721 NMIRSESTYCIROYAVVRDSDGQVHKSFRRQVTTLSLQPYMGQFLKHLDSDASALR 780
Db 721 NMIRSESTYCIROYAVVRDSDGQVHKSFRRQVTTLSLQPYMGQFLKHLDSDASALR 780
Qy 781 NSWVIEQSIWNNESSSLDFDLFLHLSVSVKIGDRCTYCCQGIPOGSSLSLTLCSLFCG 840
Db 781 NSWVIEQSIWNNESSSLDFDLFLHLSVSVKIGDRCTYCCQGIPOGSSLSLTLCSLFCG 840
Qy 841 DMENKLFARVQDGLLLRFVDDFLVTPHLDQAKTFLSTLVHGVPEYGCMLNLTQVNF 900
Db 841 DMENKLFARVQDGLLLRFVDDFLVTPHLDQAKTFLSTLVHGVPEYGCMLNLTQVNF 900
Qy 901 PVEPTLGGAAEYQLPALCHLFWCGLLDTOTLEVPDYSYGAQTSIKTSLTFQSVFKAG 960
Db 901 PVEPTLGGAAEYQLPALCHLFWCGLLDTOTLEVPDYSYGAQTSIKTSLTFQSVFKAG 960
Qy 961 KTRMKNLSVLKCHGLFLDQVNSLQVVCINIYKIFLQAYRFHACVQLPFPQVRK 1020
Db 961 KTRMKNLSVLKCHGLFLDQVNSLQVVCINIYKIFLQAYRFHACVQLPFPQVRK 1020
Qy 1021 NLTFFLGISSQASCCYAILKVNPGMTLKASGSPPEAAHWLCYQAFLLKLAHSVIYK 1080
Db 1021 NLTFFLGISSQASCCYAILKVNPGMTLKASGSPPEAAHWLCYQAFLLKLAHSVIYK 1080
Qy 1081 CLLGPLRTAQKLLCRKLPEATWTILKAAADPALSTDFQITLD 1122
Db 1081 CLLGPLRTAQKLLCRKLPEATWTILKAAADPALSTDFQITLD 1122

RESULT 3
ABB06711
ID ABB06711 standard; protein; 1122 AA.
XX
AC ABB06711;

XX 11-JUN-2002 (first entry)
XX Mouse telomerase protein sequence.
XX
XX Mouse; telomerase; promoter; telomerase catalyst subunit; TERT; mTERT;
KW enzyme; transgenic mouse; drug development; anticancer.
XX
XX Mus sp.
XX JP2002000121-A.
XX
XX 08-JAN-2002.
XX
XX 23-JUN-2000; 2000JP-00190137.
XX
XX 23-JUN-2000; 2000JP-00190137.
XX
XX (RIKO-) ZH RIKOGAKU SHINKOKAI.
PA (KIRI) KIRIN BREWERY KK.
XX
XX WPI; 2002-298279/34.
XX
XX A transgenic mouse comprising a DNA promoter region of mouse telomerase
PT catalyst subunit (TERT) is used for the development of drugs and
PT anticancer agents for regeneration of tissues and organs.
XX
XX Disclosure; Fig 3; 13pp; Japanese.
XX
XX The present invention describes a transgenic mouse (I) comprising a DNA
CC construct having a DNA containing a promoter region of mouse telomerase
CC catalyst subunit (TERT) and a DNA containing a reporter gene connected
CC under the control of the promoter region. The transgenic mouse can be
CC used in the development of drugs and anticancer agents for regeneration
CC of tissues and organs. The present sequence represents the mouse
CC telomerase protein, which is given in the exemplification of the present
CC invention
XX
XX Sequence 1122 AA;
SQ
Query Match 99.2%; Score 5854; DB 5; Length 1122;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1115; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 MTRAPRCFAVASLRLSRVREVMPLATFVRRLGPEGRRLVQPGDPKIRYTLVAQCLVCMHW 60
Db 1 MTRAPRCFAVASLRLSRVREVMPLATFVRRLGPEGRRLVQPGDPKIRYTLVAQCLVCMHW 60
Qy 61 GSQPPADLSFHQVSSSLKELVARVVQRLCERNERNVLAFGPELLNEARGGPPMAFTSSVR 120
Db 61 GSQPPADLSFHQVSSSLKELVARVVQRLCERNERNVLAFGPELLNEARGGPPMAFTSSVR 120
Qy 121 SYLNTVETLRVSGAWMLLSRVGDDLLVYLAHCALYLLPVPSCAYQVCGSPLYQICA 180
Db 121 SYLNTVETLRVSGAWMLLSRVGDDLLVYLAHCALYLLPVPSCAYQVCGSPLYQICA 180
Qy 181 TTDIWPVSASVYRTPRPGVGRNTNLRFLQOIKSSSRQEAPEKPLALPSRGTKRHLSLTSTS 240
Db 181 TTDIWPVSASVYRTPRPGVGRNTNLRFLQOIKSSSRQEAPEKPLALPSRGTKRHLSLTSTS 240
Qy 241 VPSAKKARCYPPRVVEEGPHRQVLPTPSGKSWPSPARSPVPTAEKOLSSKGKVDLSL 300
Db 241 VPSAKKARCYPPRVVEEGPHRQVLPTPSGKSWPSPARSPVPTAEKOLSSKGKVDLSL 300
Qy 301 SGSVCKKHKPSSTLSLSPRONAFQLRPFETRHFLYSRGDQERLNPFLSNLPNLT 360
Db 301 SGSVCKKHKPSSTLSLSPRONAFQLRPFETRHFLYSRGDQERLNPFLSNLPNLT 360
Qy 361 GARRLVEIIFLGSRRPRTSGPLCRTHLSRRYQWMPPLFOQLLVNHAECQYVRLLSHCRF 420
Db 361 GARRLVEIIFLGSRRPRTSGPLCRTHLSRRYQWMPPLFOQLLVNHAECQYVRLLSHCRF 420
Qy 421 RTANQOQVTDALNTSPHMLDLRLHSSPMQVYGFRLACLCCKVVSASLWGTNRNRRFPKN 480

421 RTANQVTDALNTSPHLLMDLRLHSSPWQYVGFRLACLCKVVSASLWGTREHRRFPKN 480
 481 LKXFTSLGKYKLSLQELMWKVEDCHWLSSPGKDRVPAAEHRLRRIIATFLFWLMD 540
 481 LKXFTSLGKYKLSLQELMWKVEDCHWLSSPGKDRVPAAEHRLRRIIATFLFWLMD 540
 541 TVVOLLRSFFVITESTQKRLFPYRKSVKLSQISGVROHLRVRRLRELSQSEVRHQ 600
 541 TVVOLLRSFFVITESTQKRLFPYRKSVKLSQISGVROHLRVRRLRELSQSEVRHQ 600
 601 DTWLAMPICRLRFIPKPNGLRPVNMYSMTGRALGRKQKQHFRTQRLKTLFSLMNYERT 660
 601 DTWLAMPICRLRFIPKPNGLRPVNMYSMTGRALGRKQKQHFRTQRLKTLFSLMNYERT 660
 661 KHPHLMGSSVLGMNDIYRTWAFVLVRVALDQTPRMVFKADVTCAYDAIPQGLVEVVA 720
 661 KHPHLMGSSVLGMNDIYRTWAFVLVRVALDQTPRMVFKADVTCAYDAIPQGLVEVVA 720
 721 NMIRHSESTYCIROYAVVRDSQGVHKSFRQVTTLSDLQVYMGQFLKHLQSDASALR 780
 721 NMIRHSESTYCIROYAVVRDSQGVHKSFRQVTTLSDLQVYMGQFLKHLQSDASALR 780
 781 NSVVEIQSISWNSSSLDFEFLHFLRHSVVKIGDRCYTCQGGIPQGSLSLTLCSLCFG 840
 781 NSVVEIQSISWNSSSLDFEFLHFLRHSVVKIGDRCYTCQGGIPQGSLSLTLCSLCFG 840
 841 DMENKLPFAVQRDGLLLRFVDDFLLVTPHLDQAKTFLSTLVHGVPYGCMLNLOKTVVNF 900
 841 DMENKLPFAVQRDGLLLRFVDDFLLVTPHLDQAKTFLSTLVHGVPYGCMLNLOKTVVNF 900
 901 PVEPTLGGAPYQLPAHCLFPMCGLLDQTLEVCDCYSGYAOISIKTSLTFOSVFKAG 960
 901 PVEPTLGGAPYQLPAHCLFPMCGLLDQTLEVCDCYSGYAOISIKTSLTFOSVFKAG 960
 961 KTMNKLLSVLRKCHGLFLOLVNSLQTVGCINIKIFLLQAYRPHACVIOQLPFDQVRK 1020
 961 KTMNKLLSVLRKCHGLFLOLVNSLQTVGCINIKIFLLQAYRPHACVIOQLPFDQVRK 1020
 1021 NLTPFLGIISQASCCYAILKVQNGMTLKASGPPPEAAHWLCYQAFLLKLAHSVIYK 1080
 1021 NLTPFLGIISQASCCYAILKVQNGMTLKASGPPPEAAHWLCYQAFLLKLAHSVIYK 1080
 1081 CLLGPLRTAQKLLCKLPEATWTLKAAADPALSTDFTOTILD 1122
 1081 CLLGPLRTAQKLLCKLPEATWTLKAAADPALSTDFTOTILD 1122

RESULT 4

ID ADG90609 standard; protein; 1152 AA.
 XX AC ADG90609;

DT 25-MAR-2004 (first entry)
 XX

DE TERT consensus sequence SEQ ID NO:12.
 XX

KW immune response; telomerase reverse transcriptase; TERT; cytostatic;
 KW immunostimulant; cancer; cytotoxic T cell response.
 XX

OS Unidentified.
 XX

PN WO2004002408-A2.
 XX

PD 08-JAN-2004.
 XX

PF 24-JUN-2003; 2003WO-US019844.
 XX

PR 27-JUN-2002; 2002US-0393295P.
 XX

PA (GERO-) GERON CORP.
 XX

PI Majumdar A, Ferber IA, Frolkis M, Wang Z;
 XX WPI; 2004-071946/07.
 XX
 PT Eliciting an immune response in a mammal specific for its own telomerase
 PT reverse transcriptase (TERT), useful for treating or preventing cancer,
 PT comprises administering a composition containing TERT of another
 PT mammalian species.
 XX
 PS Claim 10; SEQ ID NO 12; 44pp; English.
 XX

The invention relates to a novel method for eliciting an immune response
 in a mammalian subject that is specific for its own telomerase reverse
 transcriptase (TERT), comprising administering an immunogenic composition
 containing a protein with at least 20 consecutive amino acids of TERT of
 another mammalian species, or a nucleic acid encoding the protein. A
 composition of the invention has cytostatic, and immunostimulant
 activity. The protein or the nucleic acid encoding the protein is useful
 in the manufacture of a medicament for the treatment of cancer in a human
 or for eliciting a cytotoxic T cell response in a human.

XX Sequence 1152 AA;

Query Match 82.3%; Score 4859; DB 8; Length 1152;
 Best Local Similarity 83.2%; Pred. No. 0;
 Matches 959; Conservative 40; Mismatches 122; Indels 32; Gaps 7;

QY 1 MTRAPRCAPVRSLLRSYREVWPLATFVRRLGPEGRLVQGPDKIYRTLVAQCLVCMHW 60
 DB 1 MPRAPRCRAVRLRSHYREVLPATFVRRLGPEGRLVQGPDPAAFRALVAQCLVCPW 60
 QY 61 GSOPPPADLDFHGVSSILKELVARVQRLCERNERNVLAFGPELLNEARGGPPMAFTSSVR 120
 DB 61 GAPPPPAAPSFHQVSSLUKELVARVQRLCERNERNVLAFGPELLDARGGPPMAFTTSVR 120
 QY 121 SYLPNTVETLRVSGAWMLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180
 DB 121 SYLPNTVETLRSGAWMLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGPPLYQIGA 180
 QY 181 TTDIWPVSASVYRTPRVGRNFTNLPLOQIKSSRQEAEPKPLALPSRGTKHLSLTS 240
 DB 181 TQARPFPHASGRPRFPVGRNFTNLGFCERAWNHSVREAGVPLGLPSGAKRGGASRS 240
 QY 241 VPSAKKARCVPVRVEBGPQRVLPSPSGKSWPSPARSPEVP---TAEKDLSKGKVSVD 297
 DB 241 LPLPKAARGAAPERTPVQGSWTPSGRTRVPSDAGSPVSPARAEEDLSKGKVSVD 300
 QY 298 LSLSGSYCCCKHPSS-TSLSPPRQNAFQLRP-FIETRHFLYSGDGOERLNPFLLSNL 355
 DB 301 LSLSGSYCCCKHPSSPPSLSSPPRPAFQLRPVVAETKHFLYSYG-GRERLRPSFLLSNL 359
 QY 356 QPNLTGARRLVEIFLGSRRPTSGPLCRTHLSRRYQWMPFLFQOLLVNHAECCYVRLLR 415
 DB 360 QPSLTGARLIVETIFLGSRRPTSGPLCRTHLSRRYQWMPFLFQELLGNHARCYPVRLLR 419
 QY 416 SHCFRTANQQVTDALNTSP-----HLMDDLRLHSSPWQYVGF 455
 DB 420 SHCFRLAAATPVAGALNTSPQGSVAAPBEVAAPQEQTDSTRMLQLRSHSSPWQYVGF 479
 QY 456 RACLCCKVVSASLWGTREHRRFPKNLKFISLGKYKLSLQELMWKVEDCHWLRSPPG 515
 DB 480 RACLCCKLVPPGLNGSRHNRFFLNKVKKFSISGKXKLSLQELTWKMKVDCAWLRSSPG 539
 QY 516 KDRVPAAEHRLRERILA---TFLFWLMDTVVOLLRSFFVITESTFQKRLFFYRKSVWS 572
 DB 540 YESVPAAEHRLRERILAKEHPFLFWLMSVVVELLSFFVITESTFQKRLFFYRKSVWS 599
 QY 573 KLOSIGVROHLRVRRLRELSQSEVRQHQEAWPAMPICRLRFIPKPNGLRPTVNMYSNGT 632
 DB 600 KLOSIGVROHLRVRRLRELSQSEVRQHQEAWPAMPICRLRFIPKPNGLRPTVNMYSNGT 659
 QY 633 RALGRRKQAOHFTQRLKTLFSLMNYERTKHPHLMGSSVLGMNDIYRTWAFVLVRVALDQ 692

Db 660 RAFGRKQAHQHTQRTKTLFVSVLNTERTKPHLLGASVLGMNDIVRTWRTFVLRVALDP 719
 Qy 693 TPRMVFVADVTGAYDAIPQGLVEVAMIRHSESTYCIQYAVVRDSDQOVHKSFR 752
 Db 720 TPRMVFVADVTGAYDAIPQGLVEVAMIRHSESTYCIQYAVVRDSDQOVHKSFR 779
 Qy 753 QVTTLSDLQPYNGQFLKHLQSDASALRNSVVEIQSISWNESSSLFDFFLHRSVVK 812
 Db 780 QVTTLSDLQPYNGQFLKHLQSDASALRNSVVEIQSISWNESSSLFDFFLHRSVVK 839
 Qy 813 IGDCVTCQGGIPQSSSLTLCSCFCGDMENKLPFAVORDGLLRFDVDDFLVTPHLDQ 872
 Db 840 IGRCVTCQGGIPQSSSLTLCSCFCGDMENKLPFAVORDGLLRFDVDDFLVTPHLDQ 899
 Qy 873 AKTFSLTVHGVPEYGCMLNKTQVNVFVPEFTLGGAPYQLPAHCLFPWCGLLDQT 932
 Db 900 AKTFSLTVHGVPEYGCMLNKTQVNVFVPEFTLGGAPYQLPAHCLFPWCGLLDQT 959
 Qy 933 LEVFCDSGYAOTSITSLTPOSVPKAGTKMTNKLKLVRLKCHGLFLDLQVNSLQTVCI 992
 Db 960 LEVFCDSGYAOTSITSLTPOSVPKAGTKMTNKLKLVRLKCHGLFLDLQVNSLQTVCI 1019
 Qy 993 NIYKIFLLQAVFHFACVILQLPDQVRKNLTFFLGLIISQASCCYAILKVNKPGMTLK-- 1050
 Db 1020 NIYKIFLLQAVFHFACVILQLPDQVRKNLTFFLGLIISQASCCYAILKVNKPGMTLK 1079
 Qy 1051 -ASGSFPPPEAAHWLCYQAFLLKLAHSHVYKCLLGLPLRTAOKLCKLPEATMTILKAAA 1109
 Db 1080 GNAGSFPPEAAHWLCYQAFLLKLAHSHVYKCLLGLPLRTAOKLCKLPEATMTILEAAA 1139
 Qy 1110 DPALSTDFQTILD 1122
 Db 1140 DPALSTDFQTILD 1152

RESULT 5

ADD21416
 ID ADD21416 standard; protein; 1128 AA.

AC ADD21416;

DT 15-JAN-2004 (first entry)

DE Golden hamster TERT protein related to continual cell growth.

KW continual growth; cultured cell; cyclin dependent kinase; cdk4; cdk2;
 KW cdk6; activating mutation; cell growth; cell division; cell cycle;
 KW cancer-causing agent; continual growth-induced cell; enzyme; TERT;
 KW telomerase; Golden hamster.

XX Mesocricetus auratus.

XX WO2003044169-A2.

XX 30-MAY-2003.

XX 15-NOV-2002; 2002WO-US036729.

XX 15-NOV-2001; 2001US-0334760P.

XX (UTEM) UNIV TEMPLE.

XX Reddy PE, Rane SG, Mettuss RV;

XX WPI; 2003-449813/42.

XX A composition for reversibly inducing continual growth in normal cells
 PT comprises a cyclin dependent kinase protein (e.g. cdk4, cdk2 or cdk6) or
 PT its active fragment, derivative, homolog or analog, having an activating
 PT mutation.

XX Disclosure; Page 119-121; 77pp; English.

XX

CC This invention relates to a novel composition for inducing a reversible
 CC state of a continual growth in cultured cells and comprises at least one
 CC compound comprising a cyclin dependent kinase (cdk)4, cdk2 or cdk6
 CC protein having an activating mutation. Growth and division of living
 CC cells involve a regular series of events and processes that comprise the
 CC cell cycle. Cyclin dependent kinases cdk2, cdk4 and cdk6 are involved in
 CC the control of G1, the point at which cells irrevocably commit to DNA
 CC synthesis and thus enter the cell cycle. The invention is useful in
 CC reversibly inducing continual growth in normal cells and may allow the
 CC screening of cancer-causing agents with the continual growth-induced
 CC cells. The present sequence is that of the golden hamster TERT protein.
 CC the catalytic subunit of telomerase, related to the invention. Note: Due
 CC to an error in the specification or sequence listing, the Seq ID numbers
 CC given in the disclosure do not correspond to those given in the sequence
 CC listing. It is therefore unclear which Seq ID number corresponds to which
 CC sequence and exactly which sequence is being claimed.

SQ Sequence 1128 AA;

Query Match 80.5%; Score 4751; DB 7; Length 1128;
 Best Local Similarity 80.1%; Pred. No. 0;

Matches 904; Conservative 90; Mismatches 127; Indels 8; Gaps 4;

Qy 1 MTRAPRCAPVRSLLASRYEVWPLATFVRRLGPEGRRLVQPDPKIYRTIVAQCILCHW 60
 Db 1 MTRAPRCAPVRSLLASRYEVWPLATFVRRLGPEGRRLVQPDPKIYRTIVAQCILCHW 60
 Qy 61 GSQPPADLSFHQVSSSLKELVARVQVRLCERNERNVLAFFPELLNEARGPMAFTSSVR 120
 Db 61 DSQPPADLSFHQVSSSLKELVARVQVRLCERNERNVLAFFPELLNEARGPMAFTSSVR 120
 Qy 121 SYLPTNTVIETLRVSGAMMLLSRVGDDLLVYLLAHFALCALYLLVPPSCAYQVCGSPYQICA 180
 Db 121 SYLPTNTVIETLRVSGAMMLLSRVGDDLLVYLLAHFALCALYLLVPPSCAYQVCGSPYQICA 180
 Qy 181 TTDIWPVSASRYRTPRVGRNFTNRLFLQTKSSSRQBAPEALPSRGTKHLSLTSTS 240
 Db 181 TAETWPSVSRIYRTPRVGRNFTNRLFLQTKSSSRQBAPEALPSRGTKHLSLTSTS 240
 Qy 241 VPSAKKACVYVPRVVEGPHRQVLPSPGSKWSPSPARSPEVP--TAEKOLSSSGKGVSD 297
 Db 241 VPSKAKACVYVPRVVEGPHRQVLPSPGSKWSPSPARSPEVP--TAEKOLSSSGKGVSD 297
 Qy 298 LSLSGSVCKHKPSSTSLSPRQNAFQRLPFIEIETRHFLYSRGDQGERLNSFLSNLQ 357
 Db 301 LSRSGSVCKHKPSSTSLSPRQNAFQRLPFIEIETRHFLYSRGDQGERLNSFLSNLQ 360
 Qy 358 NLTGARLVEILFLGSRRTSGPLCRTHLSRRVWQMRPLFQOLLVNHAEQYVRLRSH 417
 Db 361 SLTGARLVEILFLGSRRTSGPLCRTHLSRRVWQMRPLFQOLLVNHAEQYVRLRSH 420
 Qy 418 CRFTANQOQVTDALN-TSPPHLMDLLRLHSSPWQVYGFRLACLCVVSASLWGTNRNRR 476
 Db 421 CRFTANQOQVTDALN-TSPPHLMDLLRLHSSPWQVYGFRLACLCVVSASLWGTNRNRR 480
 Qy 477 FFKNLKPFISLGKYGKLSLQELMWKQVYEDCHWLRSSPGKDRVPAAEHRLRERILATFL 536
 Db 481 FFKNLKPFISLGKYGKLSLQELMWKQVYEDCHWLRSSPGKDRVPAAEHRLRERILATFL 540
 Qy 537 WMDTVVQLLRSPFYITESTFQKRLPFYKYSWKSQSGVROHLRRLRRLRSLQSEV 596
 Db 541 WMDTVVQLLRSPFYITESTFQKRLPFYKYSWKSQSGVROHLRRLRRLRSLQSEV 600
 Qy 597 RHHODTWLAMPICRLRFPKPNGLRPIVNMYSYMGTRALGRKQAHQHTQRTKTLFSLN 656
 Db 601 RHHODTWLAMPICRLRFPKPNGLRPIVNMYSYMGTRALGRKQAHQHTQRTKTLFSLN 659
 Qy 657 YERTKPHLMGSSVLGMNDIVRTWRTFVLRVALDQTPRMTYFVKADVTGAYDAIPQGLV 716
 Db 660 YELTKHTNLLGASVLGMNDIVRTWRTFVLRVALDQTPRMTYFVKADVTGAYDAIPQGLV 719
 Qy 717 EVVANMIRHSESTYCIQYAVVRDSDQOVHKSFRQVTTLSDLQPYNGQFLKHLQSDA 776

Db 720 EVIANMIRHSDNSYCIHOYAVVQRDRQCIHKSFRRQVSTLSLQPHMGQFLKHLQSDT 779
Qy 777 SALRNSVVEIQSISWNESSSLPFFFLHFLRHSVVKIGDRCYTCOGIPQSSSLTLLCS 836
Db 780 SALRNSVVEIQSLNEASSSLPFFFLRFRVNSVVKIGRCYVQCQIPQSSSLTLLCS 839
Qy 837 LCFGDMENKLFABVQRDGLLRFDVDFLLVTPHLDQAKTFLSLTVHGVPEYGCMINLQKT 896
Db 840 LCFGDMENKLFABVQDGLLRFDVDFLLVTPHLDQAKTFLSLTVHGVPEYGCMINLQKT 899
Qy 897 VVNFPEVETGGAAPIYQALPAHCLFPMWGLLDDTQTLLEVFCYDGYAQTSTIKTSLTFQSV 956
Db 900 VVNFPEVADGTLDTAGPHQLPAHCLFPMWGLLDDTQTLLEVLCYDTGYARTSISAKSLTFQRT 959
Qy 957 FKAGKTMKLLSVLRKCHGLFLDLQVNSLQTVICINIKIFLQAFHACVQLPDPQ 1016
Db 960 FKAGRNMRQKLLAVLRKCHSLFLDLQVNSLQTVICINIKIFLQAFHACVQLPDPQ 1019
Qy 1017 RVRKNLTPFLGIISSQASCCYAILKVNPGWTLK---ASSGSPFPPEAAHWLCYQAFLLKLA 1073
Db 1020 HVRKNPAFFLSIINIASCCYSILKVNAGWTLKAKAGSGFPPEAAHWLCYQAFLLKLA 1079
Qy 1074 AHSVIYKCLLGLRTAQKLCRKLPEATMTILKAAADPALSTDFQTILD 1122
Db 1080 GHSVYKCLLGLRTAQKLCRKLPRATWATILETAADPALSTDFQTILD 1128

RESULT 6
ADG90603
ID ADG90603 standard; protein; 1128 AA.

XX AC ADG90603;

XX DT 25-MAR-2004 (first entry)

XX DE Hamster TERT SEQ ID NO:6.

XX KW hamster; immune response; telomerase reverse transcriptase; TERT;
XX KW cytosolic; immunostimulant; cancer; cytotoxic T cell response.

XX OS Mesocricetus auratus.

XX PN WO2004002408-A2.

XX PD 08-JAN-2004.

XX PF 24-JUN-2003; 2003WO-US019844.

XX PR 27-JUN-2002; 2002US-0393295P.

XX PA (GERO-) GERON CORP.

XX PI Majumdar A, Ferber IA, Frolkis M, Wang Z;

XX DR WPI; 2004-071946/07.

XX DR N-PSDB; ADG90602.

XX PT Eliciting an immune response in a mammal specific for its own telomerase
XX PT reverse transcriptase (TERT), useful for treating or preventing cancer,
XX PT comprises administering a composition containing TERT of another
XX PT mammalian species.

XX PS Claim 10; SEQ ID NO 6; 44pp; English.

XX The invention relates to a novel method for eliciting an immune response
XX in a mammalian subject that is specific for its own telomerase reverse
XX transcriptase (TERT), comprising administering an immunogenic composition
XX containing a protein with at least 20 consecutive amino acids of TERT of
XX another mammalian species, or a nucleic acid encoding the protein. A
XX composition of the invention has cytostatic, and immunostimulant
XX activity. The protein or the nucleic acid encoding the protein is useful
XX in the manufacture of a medicament for the treatment of cancer in a human
XX or for eliciting a cytotoxic T cell response in a human.

XX SQ Sequence 1128 AA;
Query Match 80.5%; Score 4751; DB 8; Length 1128;
Best Local Similarity 80.1%; Pred. No. 0;
Matches 904; Conservative 90; Mismatches 127; Indels 8; Gaps 4;
Qy 1 MTRAPRCPA VRSLLRSYREVWPLATFVRRLGPEGRRLVQGPDKIYRTLVLAOCLVCMHW 60
Db 1 MPRAPRCRA VRLRSQYRVWPLATFVRRLGPEGRRLVQGPDKIYRTLVLAOCLVCMHW 60
Qy 61 GSQPPADLSL FHFQVSSILKELVARVQRLCERNERNVLAFGFELLNEARGPMAFTSSVR 120
Db 61 DSQPPADLSL FHFQVSSILKELVARVQRLCERNERNVLAFGFELLNEARGPMAFTSSVR 120
Qy 121 SYLPNTVETLRVSGAWMLLSRVGDDLLVYLALHACALYLLVPPSCAYQVCGSPLYQICA 180
Db 121 SYLPNSVTESLRVSGAWMLLSRVGDDLLVYLALHACALYLLVPPSCAYQVCGSPLYQICA 180
Qy 181 TTDIWPSVAS YRPTRVGRNFTNLRFLOQIKSSSRQEA PKPLALPSRGTKRHLSTSTS 240
Db 181 TASTWPSVSI YRPTRVGRNFTNLRFLOQIKSSSRQEA PKPLALPSRGTKRHLSTSTS 240
Qy 241 VPSAKKARCY PVRVEBGPQRVLPTPSGKSWPSPARSPEVP---TAEKDLSSKGKVD 297
Db 241 VPSKAKRCDL APRLEKGPYRQAVPTPSDXTWVPNPAKSHAVPISTRTTKEDLSSGVKAPG 300
Qy 298 LSLSGSVCCG KPSSTSLSPPRQNAFQLRPFITRHFPLYSRGDQGRINPSPFLSNLQ 357
Db 301 LSRSGSVCYK HPSSTSLSPQLCQNAFQLRPFITRHFPLYSRGDQGRINPSPFLSNLQ 360
Qy 358 NLTCARLVEI IFLGSRPRTSGPLCRTHLSRRYQWQRPFLQOLLVNHAEQVYRLLRSH 417
Db 361 SLTGARKLVEI IFLGSRPRTSGPLCGRRRLSKRYQWQRPFLQOLLVNHAEQVYRLLRSH 420
Qy 418 CRFRTANQVTDALN-TSPPHLMDLLRLHSSPMQVYGFRLRACLCCKVVSASLWGTNRHRR 476
Db 421 CRFRTAAHQVAGALNTTSPQRLANLLRLHSSPMQVYGFRLRACLCCKVVSASLWGTNRHRR 480
Qy 477 FPKNLKFI SLGKYGKLSLQELMWMKVEDCHLRSRSGKDRVDPAAHRLRERILANFLF 536
Db 481 FFKNVKRFI SLGKYDKLSLQELTWQMKVQDCRLRSSPQNNCPVPAASHRTREIRLAVFLF 540
Qy 537 WLMDTVVQLLRGFFYITESTFOKNRLFYKRSVMSKLSIGVQRHLERLRLSREB 596
Db 541 WLMDAYVVELLRGFFYITESTFOKNRLFYKRSVMSKLSIGVQRHLERLRLSREB 600
Qy 597 RHHQDTWLAMPI CRLRPIPKPGLRPIVNMYSNGTALGRRKQAQHTQRLKTLFSLMLN 656
Db 601 RQREAWPAMPI CRLRPIPKPGLRPIVNMYSNGTALGRRKQAQHTQRLKTLFSLMLN 659
Qy 657 YERTKPHLMGSSVLGNDDIYRTWRAPLVRLALDQTPRMVFKVADVTGAYDAIPQDKLV 716
Db 660 YELTKHTNLGASVLGNDIYRTWRAPLVRLALDQTPRMVFKVADVTGAYDAIPQDKLV 719
Qy 717 EVVANMIRHSESTYCIROYAVVRRDSQGVHKSPRRQVTTLSLQPYMGQFLKHLQSDA 776
Db 720 EVIANMIRHSDNSYCIHOYAVVQRDRQCIHKSFRRQVSTLSLQPHMGQFLKHLQSDT 779
Qy 777 SALRNSVVEIQSISWNESSSLPFFFLHFLRHSVVKIGDRCYTCOGIPQSSSLTLLCS 836
Db 780 SALRNSVVEIQSLNEASSSLPFFFLRFRVNSVVKIGRCYVQCQIPQSSSLTLLCS 839
Qy 837 LCFGDMENKLFABVQRDGLLRFDVDFLLVTPHLDQAKTFLSLTVHGVPEYGCMINLQKT 896
Db 840 LCFGDMENKLFABVQDGLLRFDVDFLLVTPHLDQAKTFLSLTVHGVPEYGCMINLQKT 899
Qy 897 VVNFPEVETGGAAPIYQALPAHCLFPMWGLLDDTQTLLEVFCYDGYAQTSTIKTSLTFQSV 956
Db 900 VVNFPEVADGTLDTAGPHQLPAHCLFPMWGLLDDTQTLLEVLCYDTGYARTSISAKSLTFQRT 959
Qy 957 FKAGKTMKLLSVLRKCHGLFLDLQVNSLQTVICINIKIFLQAFHACVQLPDPQ 1016
Db 960 FKAGRNMRQKLLAVLRKCHSLFLDLQVNSLQTVICINIKIFLQAFHACVQLPDPQ 1019

Db 960 FKAGRNMRQKLLAVLRKCHSLFLDLQMSLQTVNCVYKIFLQAYRFHACALQPPDQ 1019
 QY 1017 RVKRLTFFLGIISQASCCYAILKVNPKQWILK---ASGSPPEAAHWLCYQAFLLKLA 1073
 Db 1020 HVEKNPAFFLSIISNTASCYSILKYNAGWILKAGGASGPPPEAAHWLCYQAFLLKLA 1079
 QY 1074 AHSVYKCLLGLPRTAQKLLCRKLPEATWILKAAADPALSTDFQILD 1122
 Db 1080 GHSVYKCLLGLPRTAQKLLCRKLPRATWMAILETAADPALSTDFQILD 1128

RESULT 7

AAW46957

ID AAW46957 standard; protein; 1132 AA.

AC AAW46957;

XX 13-AUG-1998 (first entry)

DT Human telomerase reverse transcriptase.

DE Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
 KW cell proliferation; cancer; ageing; ribonucleoprotein.

XX Homo sapiens.

XX GB2317891-A.

XX 08-APR-1998.

XX 01-OCT-1997; 97GB-00020890.

XX 01-OCT-1996; 96US-00724643.

XX 18-APR-1997; 97US-00844419.

XX 25-APR-1997; 97US-00846017.

XX 06-MAY-1997; 97US-00851843.

XX 09-MAY-1997; 97US-00854050.

XX 14-AUG-1997; 97US-00911312.

XX 14-AUG-1997; 97US-00912951.

XX 14-AUG-1997; 97US-00915503.

XX (GERO-) GERON CORP.

XX (UYTE-) UNIV TECHNOLOGY CORP.

XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;

XX Andrews WH;

XX WPI; 1998-171633/16.

XX N-PSDB; AAW22379.

PT Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of cell
 PT proliferation conditions especially cancer and ageing.

XX Claim 3; Fig 17; 387pp; English.

XX The present sequence represents human telomerase reverse transcriptase
 CC (hTERT), which is a ribonucleoprotein. The present invention also
 CC describes the following methods: (A) determining whether a test compound
 CC is a modulator of hTERT, by detecting the change in hTERT recombinant
 CC protein or polynucleotide, on administration of the compound; (B)
 CC preparation of recombinant telomerase by contacting a protein preparation
 CC of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or
 CC protein in a sample by binding a relevant probe to the sample and
 CC detecting the complex formed or in the case of RNA detection, amplifying
 CC the product and correlating the presence of complex or amplification
 CC product with presence of hTERT in the sample; and (D) increasing the
 CC proliferation of a vertebrate cell by increasing hTERT expression; and (E)
 CC the use of an agent that causes an increase in cell vertebrate cell
 CC proliferation to create a medicament that inhibits ageing. A protein
 CC preparation of hTERT and the polynucleotide encoding hTERT can be used in
 CC the manufacture of medicaments for inhibiting the effect of ageing or
 CC cancer. Inhibitors of telomerase activity can be used to treat conditions

CC that are associated with high telomerase activity. A protein preparation
 CC of hTERT can also be used in the new methods

SQ Sequence 1132 AA;

Query Match 59.4%; Score 3505; DB 2; Length 1132;

Best Local Similarity 62.4%; Pred. No. 0;

Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;

QY 1 MTRAPRCAPVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPDGPKIYRTLVQAQCLVCMHW 60

Db 1 MPRAPRCAPVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPDGPKIYRTLVQAQCLVCMHW 60

QY 61 GSQPPPADLSFHQVSSSLKELVARVYQRLCERNERNVLAFGFELLNEARGGPPMAFTSSYR 120

Db 61 DARPPPAAPSFRQVSLAKELVARVYQRLCERNERNVLAFGFELLNEARGGPPMAFTSSYR 120

QY 121 SYLPTVETLRVSGAWMLLSRVGDDLLVYLAHCALYLLVPPSCAYQVCSPLYQICA 180

Db 121 SYLPTVETLRVSGAWMLLSRVGDDLLVYLAHCALYLLVPPSCAYQVCSPLYQICA 180

QY 161 TTDIWPVSASVYRTPVPGRNFTNLRFLOQIKSSSRQAPKPLALPSRGTKRHLSLTSTS 240

Db 161 ATQARPPPHAS-GPRRLG-----CERAWNHSVREAGVPLGLPAPCARRGGSASRS 231

QY 241 VPSAKKARCYVPVRVEEGP-----HRQVLPTPSGKSW-VPSPARSPREVPTAEKDLSSK 292

Db 232 LPLPKRPRGAAPERTPVGGSWAHFGRTGSDRGFCVVSAR-----PAEATSLE 286

QY 293 GKVDLSLS-GSVCKHKPSSTLSLSPRONAQLRP-FIETRHFLYSGDQGRRLNPSF 350

Db 287 GALSGRHSHPSVGRQHAGPPSTSRPDPMDTTPCPVVAETKFLYSSGD-KEQLRPSF 345

QY 351 LLSNLQPNLTGARLVEIIFLGSRRPTSGPLCRTHLSRRYQWMPPLFQOLLVNHAEQY 410

Db 346 LLSLRPLSLTGARLVEIIFLGSRRPTSGPLCRTHLSRRYQWMPPLFQOLLVNHAEQY 405

QY 411 VLLRSHCRFTANQQVTDAL-----NTSPPHMLDMLLRHSSPFWQVY 452

Db 406 GVLLKTHCPLEAA---VTPAAGVCAREKPGQSVAAPEEDTDPRLVQLLRQSSPFWQVY 462

QY 453 GFLRACLCKVVSASLWGTTRHNRFFKNLKKFISLGKYKGLSLQELMWMKVEDCHWLSR 512

Db 463 GFVRACLRLVPPGLWGSRHNRFFLNRTKKFISLGKHAQLSLQELTWKMSVRDCAWLRR 522

QY 513 SPGKDRVPAAEHRLAERILATFLWMDTYVOLLRSFFYITESTFQKNRPLFFYKRSVMS 572

Db 523 SPGVCVPAAEHRLAERILATFLWMDTYVOLLRSFFYITESTFQKNRPLFFYKRSVMS 582

QY 573 KLSQISGVROHLERVRLRELSOEVRHHODTWLAMPICRLRFPKNGRLPVMNSYSMTG 632

Db 593 KLSQISGVROHLERVRLRELSOEVRHHODTWLAMPICRLRFPKNGRLPVMNSYSMTG 642

QY 633 RALGRKQAOHFTQRLKTLFSKMLNYERTKPHLMGSSVILGMNDIYRTWRAFLVRALDQ 692

Db 643 RTFRREKKAERLTSKVKALFVNLVYERARRPCLLGASVLGLDDIHRAWRTFVLVRAQDP 702

QY 693 TPRMYFVKADYTGAYDAIPQKLVVEVVMNTHSESTYCIQYAVVRDSDSQGVHKSFR 752

Db 703 PPELYFVKVDYTGAYDTIPQDLRLTEVIAIHK-PQNTYCVRYAVVQAAHGHVRAKPKS 761

QY 753 QVTTLSDLQPYMGQFLKHLQSDASALRNSVVEQSISMNESSSLPFFLHFLHRSVVK 812

Db 762 HVSTLTDLPYMGQFLKHLQSDASALRNSVVEQSISMNESSSLPFFLHFLHRSVVK 819

QY 813 IGDCRYTCQCGIPQSSSLTLLCSLCFGDMENKLFPAEQVRDGLLRLRVDDFLVTPHLQ 872

Db 820 IRGKSYVQCGIPQSSSLTLLCSLCFGDMENKLFPAEQVRDGLLRLRVDDFLVTPHLQ 879

QY 873 AKTFSLTLVHGVPEYGCMLNOKTVNPPBPGLTGAAPYQLPAHCLFPWCGLLLDQTQ 932

Db 880 AKTFSLTLVHGVPEYGCMLNOKTVNPPBPGLTGAAPYQLPAHCLFPWCGLLLDQTQ 939

Qy	1053	GS----	FPPEAAHWLCYQAFILKLAHSHVIYKCLIGPLRTAQKLCRKLPEATMTILKAAA	1109
		:		:
Db	1060	GAAGPLPSEAVQWLCHQAFLLKLTTRHRVTYVPLLGSLRTAQQLSRKLPGLTTLTALEAAA	1119	
		:		:
Qy	1110	DPALSTDPQTILD	1122	
		:		:
Db	1120	NPALPSPDKTILD	1132	
RESULT 10				
AA32090.				
ID	AA32090 standard; protein; 1132 AA.			
XX	AA32090;			
XX	AC			
DT	17-JAN-2000 (first entry)			
XX	Human telomerase reverse transcriptase (hTERT).			
DE				
KW	Telomerase reverse transcriptase; human; hTERT; cell proliferation; cancer.			
KW				
XX	Homo sapiens.			
OS				
XX	W0950386-A2.			
PN				
XX	07-OCT-1999.			
PD				
XX	31-MAR-1999; 99WO-US007097.			
PP				
XX	31-MAR-1998; 98US-00052864.			
PR	03-AUG-1998; 98US-00128354.			
FR				
XX	(GERO-) GERON CORP.			
PA				
XX	Morin GB;			
PI				
XX	WPI; 1999-610842/52.			
DR	N-PSDB; AA220279.			
DR				
PT	New catalytic polypeptide and polynucleotide, useful for increasing catalytic activity in a cell.			
PT				
XX	Claim 13; Fig 1; 24pp; English.			
PS				
XX				
CC	The present sequence represents human telomerase reverse transcriptase (hTERT). Human telomerase is a target for diagnosing and treating diseases relating to cell proliferation and senescence, such as cancer, or for increasing the proliferative capacity of a cell. A claimed method for increasing the proliferative capacity of a vertebrate cell, especially a human or other mammalian cell, involves introducing into the cell a recombinant hTERT polynucleotide encoding an hTERT variant in which residues 192-323, 200-323, 192-271, 200-271, 222-240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 of the present sequence are deleted. A claimed method of preparing recombinant telomerase involves contacting a recombinant hTERT deletion mutant (as above) with a telomerase RNA component such that the 2 proteins associate to form a complex capable of catalyzing the addition of nucleotides to a telomerase substrate. A claimed method for reducing telomerase activity in a cell involves introducing a recombinant polynucleotide encoding an hTERT variant having a deletion of amino acids 192-450, 560-565, 637-660, 748-764 or 1055-1071 of the present sequence			
CC				
XX	Sequence 1132 AA;			
Query Match				
Best Local Similarity 59.4%; Score 3505; DB 2; Length 1132;				
Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;				
Qy	1	MTRAPRCVARSLLRSRYREVWPLATFVRRLLGPEGRRVLVQPGDPKRYRTLVAQCLVCMHW	60	
Db	1	MTRAPRCVARSLLRSRYREVWPLATFVRRLLGPEGRRVLVQPGDPKRYRTLVAQCLVCMHW	60	

Qy	61	GSOPPPADLSFHVSSIKELVARVWORLCEBNNRNLAFGFFELNLRARGGPPMAFTSSVR	120
Db	61	DARPPAAPSPFQVSCLEKELVARVQRLCERGAKNVLAFCFALLDARGGPPFAFTTSVR	120
Qy	121	SYLPNTVETLRVSGAWMLLSRVGDDLLVYLLAHACALYLLVPPSPCAVQVCGSPLYQICA	180
Db	121	SYLPNTVTDALRGSGAWMLLSRVGDDVLVHLLARCALFVLVAPSCAVQVCGPPLYQLGA	180
Qy	181	TTDIWPSVSAYRPTRPVGRNFTNLRFLOQIKSSSQEAPKPLALPSRCTKHLSTLSTS	240
Db	181	ATQARPPPHAS-GPRRRLG-----CERAWHVSREAGVPLGLPAPGARRRGGSASRS	231
Qy	241	VPSAKKARCYVPVRVEGP-----HRQVLPTPSGKSM-VPSPARSPVEPTAKDKLSSK	292
Db	232	LPLPKPRRGAAPERTPVGQSGSWAHGTRGSPDRGFCVSPAR-----PAEATSLSE	286
Qy	293	GKVSLSLS-GSVCKHKPSSTLSLGGPPRONAFQLRP-FIETRHFLYSRGDQGRLNPSF	350
Db	287	GALSGTSHSPSVGRQHAGPPSTSRPPRPMDTPCPDVAETKHFLYSSGD-KEQLRPSF	345
Qy	351	LLNLQNLTGARRLVEIIFLGSRPSTSGPLCRTHLSRRYWMRPLFQOLLVNHACQY	410
Db	346	LLSLRPSLTGARRLVETIFLGSRPMPGTPRRLPLRPQRYWMRPLFLELLGNHACQY	405
Qy	411	VRLLRSHCRPTANQQVTDAL-----NTSPPHLMDLLRLHSSPMQVY	452
Db	406	GVLLKTHCPURAA---VTPAAGVCAREKPGQSVAAPEEDTDPRLLVQLLRQHSSPMQVY	462
Qy	453	GFLRACLCKVVSASLMGTRHNRERFFKXKFTSLGKYKLSLQELMKMKVEDCHWLRS	512
Db	463	GFVRACLRRLVPPCLGWSRNRERFLRNTKFTISLGKHAKLSLQELTKMSVRDCAWLRR	522
Qy	513	SPGKDRVPAAEHLRERILATFLFWMMDTVVOLLSPFFVITESTFOKRLFFYRKSVMS	572
Db	523	SPGVGCVPAAEHLRERILAKFLHLSVVVVELLSFFVYVTFTFOKNRLFFYRKSVMS	582
Qy	573	KLOSIGVROHLRVLRLRELSQEEVRHODTWLAMPICRLRPIPKPNCGLRPIVNNMSWGT	632
Db	583	KLOSIGIRQHLKRVQLRELSAEVRQREARPPALLTSRLRPIPKPDGLRPIVNDVVUGA	642
Qy	633	RALGRRKQAOHQRTQRLKTLFSLNRYERTKPHLMGSSVLGMNDIYRTWRAPVLVRALDQ	692
Db	643	RTFRERKRAERLTSRVKALFSLNRYERARRPGLLGASVLGLDDIHRARWTFVLVRADP	702
Qy	693	TPRMVFKADVGTAYDAIPQGLVVEVANNIRHSESTYCIQYAVVRDSDGQVHKSPRR	752
Db	703	PPELYFVKVDVTGAYDTIPQDLRTEVIAIHK-PONTYCVRRYAVVQKAAHGHVKKAFKS	761
Qy	753	QVTTLSDLQPMVGQFLKHLQSDASALRNSVVIQSIISMNNESSSLDFFLHFLRHSVVK	812
Db	762	HVSTLTDLPYMRQFVAHLQET--SPLRDAVVIEQSSSLNEASSGLFDVFLRFCHHAVR	819
Qy	813	IGDRCTYCCQGIPOGSSSLTLLCSLCFCDMENKLFARVQRDGLLLRVDDFLVTPHLDDQ	872
Db	820	IRGKSYVQCQGIPOGSSILTLLCSLCYCDMENKLFAGIRDRDGLLLRLVDDFLVTPHLTH	879
Qy	873	AKTFLSTLVGVPEYGCWMLNOKTVNPFVPGTGLGNAAPVQLPAHCLFPMCGLLDPTQ	932
Db	880	AKTFLRTLVRGVPEYGCWMLNOKTVNPFVDEALGGTAFVQMPAHGLFFPMCGLLDPT	939
Qy	933	LEVPCDYSVGAQTSIKTSLTFQSVFKAGKTRNKLKSLVRLKCHGLFLDLQVNSLQTVCI	992
Db	940	LEVQSDYSSVARTSIRASLTFNRGFKAGRNRKLFVGLRLKCHSLFLDLQVNSLQTVCT	999
Qy	993	NIYKIFLLQAYRFHACVQLPFDQVRNRNLTFFPIGIISSQASCCYAILKVXNPGMTLKAS	1052
Db	1000	NIYKILLQAYRFHACVQLPFPHQVWKNPTFFFLRVISDTASLCYSILKAKNAGSLGAK	1059
Qy	1053	GS----FPPEAAHWLCYQAFILKLAHSHVIYKCLIGPLRTAQKLCRKLPEATMTILKAAA	1109
Db	1060	GAAGPLPSEAVQWLCHQAFLLKLTTRHRVTYVPLLGSLRTAQQLSRKLPGLTTLTALEAAA	1119

QY	1110	DPALSTDFQTILD	1122	
DB	1120	NPALPSDFKTILD	1132	
RESULT 11				
AAAY43621				
ID	AAAY43621 standard; protein; 1132 AA.			
XX	AAAY43621;			
XX	26-JAN-2000 (first entry)			
XX	A human telomerase reverse transcriptase (TRT) polypeptide.			
DE	Human; telomerase reverse transcriptase; TRT; T lymphocyte activation;			
KW	dendritic cell; telomerase activity; cancer cell; proliferating cell;			
KW	immunological destruction; telomerase; cancer; proliferation disease.			
XX	Homo sapiens.			
XX	WO9950392-A1.			
XX	07-OCT-1999.			
XX	30-MAR-1999; 99WO-US006898.			
XX	31-MAR-1998; 98US-0112006P.			
XX	(GERO-) GERON CORP.			
XX	Gaeta FCA;			
XX	WPI; 1999-610845/52.			
XX	N-PSDB; AA230154.			
PT	Eliciting an in vivo immune response for prevention and treatment of			
PT	cancers.			
XX	Claim 3; Fig 1; 26pp; English.			
XX	The present sequence represents a human telomerase reverse transcriptase			
CC	(TRT) polypeptide. The protein is used in the method of the invention.			
CC	The specification describes a method for activating a T lymphocyte,			
CC	comprising contacting the T lymphocyte with a dendritic cell that			
CC	expresses a TRT peptide in the context of a MHC class I or MHC class II			
CC	molecule. The protein causes induction of an in vivo immunological			
CC	response to telomerase activity. Cancer cells are characterized by			
CC	expression of endogenous TRT gene and the presence of detectable			
CC	telomerase activity. Therefore, by eliciting a specific immune response			
CC	to TRT or to TRT-expressing cells, it is possible to selectively target			
CC	proliferating cells for immunological destruction. The method is used for			
CC	eliciting an in vivo immune response to telomerase by activating a T			
CC	lymphocyte, and is useful for prevention and treatment of cancers and			
CC	other proliferation diseases/conditions			
XX	Sequence 1132 AA;			
QY	Query Match 59.4%; Score 3505; DB 2; Length 1132;			
DB	Best Local Similarity 62.4%; Pred. No. 0;			
XX	Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;			
QY	1	MTRAPRCAPVRLSRVREYVPLATFVRLGPEGRRVQPDPKIYRTLVAQCLVCMHW	60	
DB	1	MTRAPRCARVRLSRVREYVPLATFVRLGPEGRRVQPDPKIYRTLVAQCLVCMHW	60	
QY	61	GSOPPPADLSFQVSSKELVARVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR	120	
DB	61	DARPPAPSPFQVSSKELVARVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR	120	
QY	121	SYLPTNTVETLRVSGANMLLSRVGDDLLVYLAAHCALYLVLPSPCAVQVCGSPYQICA	180	
DB	121	SYLPTNTVETLRVSGANMLLSRVGDDLLVYLAAHCALYLVLPSPCAVQVCGSPYQICA	180	

QY	1110	DPALSTDFQTILD	1122	
DB	1120	NPALPSDFKTILD	1132	
RESULT 12				
AAAY26580				
ID	AAAY26580 standard; protein; 1132 AA.			
QY	1	TTDIWPSVSASYRTRFVRGNFTNLRLFOQIKSSSRQEAQPKLALPSRGTKRHLSTSTS	240	
DB	1	ATQARPPPHAS-GPRRLG-----CERAMNHSVREAGVPLGLPAGPARRRGGASRS	231	
QY	241	VPSAKKARCYPVPRVEGPP-----HRQVLPTPSGKSW-VPSPASPEVPTAEKDLSSK	232	
DB	232	LPLKPRPRRGAAPERTPVGQSWAHPTGRGSDRGFCVGVSPAR-----PABEATSL	286	
QY	293	GKVDLSLS-GSVCCKHKPSSTLLSPRONAQLRP-FIETRHFLYSRGDGQERLNPSF	350	
DB	287	GALSGTRHSHPSVGRQHAGPSTSRPRPRWDTPCPVPVYAEHTKHFLYSSGD-KEQLRPSF	345	
QY	351	LLSNLQPNLTGARELVEIIFLGSRPRTSGPLCRTHRLSRRYQWRFLFOQLLVNHAECQY	410	
DB	346	LLSSLRPSLTGARELVETIFLGSRPMPGTPRLPRLPQRYQWRFLFLELLGNHAQCPY	405	
QY	411	VRLRSCHRCFTANQQVTDAL-----NTSPPHLMDLLRLHSSSPQVY	452	
DB	406	GVLLKTHCPLRAA---VTPAAGVCAREKPGQSWAAPFEEDTPRRLVQLLRQHSSPQVY	462	
QY	453	GFLRACICKVVSASLWGTNRERRFPKNLAKFISLQKYGKLSLQELMKMKMKVEDCHLRS	512	
DB	463	GFVRACLRRLVPPGLWGSNRERRFLRNTKCFISLQKHAKLSLQELTWKMSVRDCAWLRR	522	
QY	513	SPGKDRVPAAEHRLRERILATFLFWLMDTYVVOQLLSFFYITESTFQKRLFPYRKSVM	572	
DB	523	SPGVGCVPAAEHRLREILAKFLHMLMSVYVVELLSRFFVYETTFQKRLFPYRKSVM	582	
QY	573	KLOSIGVROHLRVRRLRELSQEVRRHQDTWLAMPICRLRFPKPNGLRPIVNMYSMGT	632	
DB	583	KLOSIGIRQHLKRVQLRELSEAEVRQREARPAALLTSRLRFPKPDGLRPIVNMVYVGA	642	
QY	633	RALGRRKQAOHPTORLKTLPESMLNYRTHKPHLMGSSVLGMNDIYRTWRAFLVRALDQ	692	
DB	643	RTPRERKARLRSRVKALFSVLYNERARRPGLGASVLGLDDIHRAMRTFVLVRQAQDP	702	
QY	693	TPRMVYFKADVGTAYDAIPQGLKLVVANNIRHSESTYCIROYAVVRRDSQGVHKSFR	752	
DB	703	PPELYFKVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRRVAVVQKAAHGHRKAFKS	761	
QY	753	QVTTLSDLQPMYQGFKLQDSDASALRNSVVTIEQISIMNNESSSLPDFPLHLRHSVVK	812	
DB	762	HVSTLTDLQPMYQFVAHLQET--SPLRDAVVTIEQSSSLNEASSGLFDVFLRFMCHHAVR	819	
QY	813	IGRCYTCOGIIPQSSSLTLLCSLCFQDMENKLPABVORDGLILRPVDDFLIATPHLQ	872	
DB	820	IRGSYVQCQGIIPQSSSLTLLCSLCYQDMENKLPAGIRDRDGLLLVLVDVDFLLVTPHLTH	879	
QY	873	AKTFLSLVHGVPYEGVMINQKTVNVPVEPGTLCGAAPYOLPAHCLFPWCGLLDTOT	932	
DB	880	AKTFLRLVHGVPYEGVCVNLRTVNVFVEDEALGTAQVQMPAGLFPWCGLLDTOT	939	
QY	933	LEVPCDYSYGAQTSIKTSLTFQSVFQKAGKTMRNKLLSVLRKCHGLFLDLQVNSLQTVCI	992	
DB	940	LEVQSDYSYVARTSIRASLTFNRRGFKAGRNMRKLFGLVRLKCHSLFLDLQVNSLQTVCT	999	
QY	993	NIYKIFLLQAYRFHACVIQLPPDQVRVKNLTTPFLGIISQASCCYAILKVKQPGMTLKAS	105	
DB	1000	NIYKILLQAYRFHACVQLPPHQQVYKQNPFFLRVISDTASLCYSILKAKNAGMSLGAK	105	
QY	1053	GS---PPPEAAHLCVQAFLKLAHSHVLYKCLLGLPLRTAQKLCCKLCPKPEATMTILKAA	110	
DB	1060	GAGPLPSEAVQVLCCHQAFLLKUTRHRVTYVPLGLSLRTAQQLSRKLPETTLTALAAA	111	
QY	1110	DPALSTDFQTILD	1122	
DB	1120	NPALPSDFKTILD	1132	
AAAY26580 standard; protein; 1132 AA.				

RESULT 12
AAY26580
ID AAY26580 standard; protein; 1132 AA.

XX AAY26580;
AC 13-SEP-1999 (first entry)
XX Human telomerase reverse transcriptase (hTERT) enzyme.
XX Telomerase reverse transcriptase; TERT; mouse; telomere length assay;
KW immunogen; enzyme; telomerase-mediated DNA replication; human.
XX Homo sapiens.
XX WO9927113-A1.
XX 03-JUN-1999.
XX 25-NOV-1998; 98WO-US025211.
XX 26-NOV-1997; 97US-00979742.
XX 16-MAR-1998; 98US-00042460.
XX (GERO-) GERON CORP.
XX (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
XX Morin GB, Allsopp R, Depinho R, Greenberg R;
XX WPI; 1999-347722/29.
XX Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and
PT nucleic acids.
XX Disclosure; Fig 3; 135pp; English.
XX The invention relates to a mouse telomerase reverse transcriptase (mTERT)
CC enzyme. Compositions containing mTERT can be used in telomere length
CC assays. Isolated mTERT is useful as an immunogen for the production of
CC monoclonal or polyclonal antibodies. The method is useful for assessing
CC the degree of purification and identification of new mTERT species, such
CC as an mTERT allele, homolog or isoform, or to screen for modulators
CC (antagonists and agonists) of telomerase-mediated DNA replication.
CC Antagonists and agonists of mTERT can be used to modify the activity of
CC other telomerase enzymes such as human TERT (hTERT). The present sequence
CC represents a human TERT enzyme
XX Sequence 1132 AA;
Query Match 59.4%; Score 3505; DB 2; Length 1132;
Best Local Similarity 62.4%; Pred. No. 0;
Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;
Qy 1 MTRAPRCVAVRSLLSRYREWFVPLATFVRLGPEGRRLVQGDPKIYRTLVAAQCLVCMHW 60
Db 1 MPRAPRCVAVRSLLSRYREWFVPLATFVRLGPEGRRLVQGDPKIYRTLVAAQCLVCPW 60
Qy 61 GSQPPADLSHYOVSSKLKELVARVQRLCERNERNVLAFGPELLNEARGGPPMAFTSSVR 120
Db 61 DARPPPAAPSRFQVSLKELVARVQRLCERNERNVLAFGPELLNEARGGPPMAFTSSVR 120
Qy 121 SYLPNTVTETLRVSGAMLLLSRVGDDLLVLLAHFALCALYLLVPPSCAYQVCGSPLYQICA 180
Db 121 SYLPNTVTDALRGSGAWGLLRVGGDDVLVLLHARFALFVLVAFSCAYQVCGSPPLYQLGA 180
Qy 181 TTDIHPVSASVSRPVRPVRGRTNRLFLQOKSSSRQAPKPLALPSRGTGRHLSLSTS 240
Db 181 ATQARPPPHAS-GPRRLG-----CERAWNHSVREAGVPLGLPAPFARRRGGSASRS 231
Qy 241 VPSAKKACYPVPRVEEGP-----HRQVLPTEPSGKSM-VPSPARSPEVFTAEDKLSK 292
Db 232 LPLPKPRRGAPEPRTFVGGGSAWHFGRTRGSDRGFCVVSPAR-----PAEATSL 286
Qy 293 GKVSLSLS-GSVCCCHKPSTSLSPRQNAFLRP-FIETRHFLYGRGDQBRANPSF 350
Db 287 GALSCTRHSHFSGVGRHQHAGPSTSRPRPMDTPCPVPVYAEKHFLYSSGD-KEQLRPSF 345

Qy 351 LLSNLPNLTGARRLVEIIFLGSRRPTSGPLCRTHLSRRYQMRPLFOQLLVNHAECQY 410
Db 346 LLSLSRPSLTGARRLVETIFLGSRRPMPGTGPRRLPRLPQRYQMRPLFELLGNHACPY 405
Qy 411 VRLRSHCRFRTANQOVTDAL-----NTSPPHLMDLLRLHSSPQVY 452
Db 406 GVLLKTHCPLRAA---VTPAAGVCAREKPOGSVAAPPEEDTDPRRLVQLLRQHSPPQVY 462
Qy 453 GFIRACLCVKVVSASLWGTNRNRRFPKLNKPFSLGKYGKLSLOELMKNKVDCHWLS 512
Db 463 GFVRACLRRLVPEGLWGRNRRFLRNTKPFSLGKHAKLSLOELTKWNSVRDCAWLR 522
Qy 513 SPGRDVRPAEHRRLRIRILATFLWLDVTYVOLLRSFFYITESTFQKNRLFYFRKSVMS 572
Db 523 SPGVGCVPAEHRRLREILAKFLHLMVSVVVELLSFFYVTTTQKNRLFYFRKSVMS 582
Qy 573 KLSIGVROHLRLRLRELSQEVRRHQDTWMLMPICLRPIPKPGLRLPIVMSVSMGT 632
Db 583 KLSIGIRQHLKRVLRELSEAEVRQREARPAALLTSRLRFIPKPDGLRPIVNDYVYGA 642
Qy 633 RALGRRKQAHFTQRLKTLFSLMNYERTKPHLMGSSVLGMNDIYRTWRAFVLVRALDQ 692
Db 643 RTERREKRAERLTSRVKALFSLNRYERARRPGLGASVLGDDDIHRAWRTFVLVRQAQDP 702
Qy 693 TPRMYFVKADVTGAYDAIPOGLVEVVANNIRHSESTYCIROYAVVRRDSQGVHKSFR 752
Db 703 PPELYFVKDVTGAYDTIPQDRLETVIASIIL-PQNTYCVRRYAVVQKAAHGVKAFKS 761
Qy 753 QVTTLSDLPYMGQFLKHLQSDASALRNSVVIQESISMNNESSSLPDPFFLHFLRHVVK 812
Db 762 HVSTLTDLPYMRQFVAHLQET--SPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAV 819
Qy 813 IGRCTYOCOGIIPQSGSLTLLCSLCFQDMENKLEAVERDGLLRFPVDDFLVTPHLQ 872
Db 820 IRGKSVYVCCGIPQSGSLTLLCSLCYGDMEKLFAGIRDRGLLRVDDFLVTPHLTH 879
Qy 873 AKTFLSTLVHGVPEYGCMLNKTQVNVFPVEPGTLAGAAPYQLPFAHCLFPWCGLLDQT 932
Db 880 AKTFLRLVRGVPEYGCMLNKTQVNVFPVEDEALGCTAFVQMPAHGLFPWCGLLDTRT 939
Qy 933 LEVFCDSYGAQTSIKTSLTFQSVFAGKTMRNKLVLRLKCHGLFLDLQVNSLQTVCI 992
Db 940 LEVQSDYSYARTSIRASLTFRNGFKAGRNMRKLFGLVRLKCHSLFLDLQVNSLQTVCT 999
Qy 993 NIYKIELLOAYRFHACVQLPDPORVKNLTFFLGIISQASCCYAILKVNKPMGLKAS 1052
Db 1000 NIYKILLLOAYRFHACVQLPDPORVKNLTFFLGIISQASCCYAILKVNKPMGLKAS 1059
Qy 1053 GS---PPEAAHMLCYQAFLLKLAHSHVIYKCLLGLPLRTAQKLCRKLPEATMTILKAA 1109
Db 1060 GAAGPLPSEAVQMLCHQAFLLKLTTRHVTYVPLLSLRTAQTLQSRKLPGLTTLTALSA 1119
Qy 1110 DPALSTDFQITLD 1122
Db 1120 NPALPSDFKITLD 1132
RESULT 13
AAG64859
ID AAG64859 standard; protein; 1132 AA.
XX AAG64859;
AC AAG64859;
XX 21-SEP-2001 (first entry)
DT Heart muscle cell differentiation related protein SEQ ID NO: 31.
XX Heart muscle cell; human; cell differentiation; heart disease.
XX Homo sapiens.
XX WO200148151-A1.
XX

XX PD 05-JUL-2001.
XX PF 27-DEC-2000; 2000WO-JP009323.
XX PR 28-DEC-1999; 99JP-00372826.
XX PR 28-FEB-2000; 2000WO-JP001148.
XX PR 02-NOV-2000; 2000WO-JP007741.
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX PI Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
PI Yamada Y;
XX DR WPI; 2001-425656/45.
XX DR N-PSDB; AAH48235.
XX CC Cells capable of differentiating into cardiomyocytes and originating in
PT bone marrow or umbilical blood cells for study of cardiomyocyte
PT differentiation and treatment of heart disease.
XX PS Claim 87; Page 143-147; 183pp; Japanese.
XX CC The present invention provides cells originating in the human bone marrow
CC or umbilical blood cells which are capable of differentiating into
CC cardiomyocytes. These cells are useful in the treatment of diseases
CC involving heart muscle degeneration, such as myocardial infarction, and
CC the study of cardiomyocyte differentiation. The present sequence is a
CC protein described in the exemplification of the invention
XX SQ Sequence 1132 AA;
Query Match 59.4%; Score 3505; DB 4; Length 1132;
Best Local Similarity 62.4%; Pred. No. 0;
Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;
QY 1 MTRAPRCRAVRSLLRSRYREVWPLATFVRRLLGPEGRRLVQPGDKIYRTLVAQCLVCMHW 60
DB 1 MPRAPCRAVRSLLRSRYREVWPLATFVRRLLGPEGRRLVQPGDKIYRTLVAQCLVCPW 60
QY 61 GSQPPADLSFHOVSLKELVARVQRLCERNERNVLAFFGPELLNEARGGPPMATSSVR 120
DB 61 DARPPPAAPSPFRQVSLKELVARVQRLCERNERNVLAFFGPELLNEARGGPPMATSSVR 120
QY 121 SYLPTNTVTLTVSGAWMLLSRGDGLLVLLAHCALVLLVPPSCAYQVCGSPLYQICA 180
DB 121 SYLPTNTVTLTVSGAWMLLSRGDGLLVLLAHCALVLLVPPSCAYQVCGSPLYQICA 180
QY 181 TTDIWPVSASVYRTPVGRNFTNLRLQOIKSSSRQEAPEKPLALPSRGTKEHLSLTSTS 240
DB 181 ATQARPPPHAS-GPRRLG-----CERAWNHSVREAGVFLGLPAPGARRGGASRS 231
QY 241 VPSAKKARCYFVPRVEGP-----HRQVLPSPGKSW-VSPSPARSPEVPTAEKDLSSK 292
DB 232 LPLKPRRGAAPPEPRTFVPGQSWAHFGRTRGSPDRGFCVVSAPR-----PAEATSLE 286
QY 293 GKVSIDLSL-GSVCKKHPSSLSLSPRQNAFLRP-FIETRHFLYSRGDQGRNLNPSF 350
DB 287 GALSSTRHSPVSGHQHAGPSTSRPPNPDWTPCPVVAETKHFYSSGD-KEQLRPSF 345
QY 351 LLSNLQPNLTGARRLVEIIFLGSRRPRTSGPLCRHLSRRYQWRPLFQQLLVNHAQCQ 410
DB 346 LLSLSRPSLTGARRLVEIIFLGSRRPRTSGPLCRHLSRRYQWRPLFQQLLVNHAQCQ 405
QY 411 VLLRSHCRFRATANOOVTDAL-----NTSPPHMLDLLLHSSPWQVY 452
DB 406 GYLLKTHCPLEAA---VTPAAGVCAREKPGQSVAAPEBEDTDPRLVQLLRHSSPWQVY 462
QY 453 GFLRACLCKVVSASLWGTTHNRRERFKNLKFKISLGYKCKLSLOELMMKVKEDCHWLS 512
DB 463 GFLRACLCKVVSASLWGTTHNRRERFKNLKFKISLGYKCKLSLOELMMKVKEDCHWLS 522
QY 513 SPGRDVRPAAEHRLERILATFLFMDTYVYVQLLRSFFYITESTFQKNRLLFFYRKSVMS 572

DB 523 SPGVGCVPAAEHRLERILAKFLHLMSSVYVVELLSPPYVVTETTFQKNRLLFFYRKSVMS 582
QY 573 KLOSGVROHLERVELRELRSQEEVREHODTWLAMPICRLRLETPKNGRLRPIVNMYSVMT 632
DB 583 KLOSGIGIQHLKRVQLRELSAEVQHREARPALITSLRFPKPDGRLRPIVNMIDYVGA 642
QY 633 RALGRKQAOHFTQRLKTLFSLMYERTKPHLMGSSVLGMDIYRTWRAPFLVRALDQ 692
DB 643 RTFREKRAERLTSRKALFSLVNYERARRPCLLGASVLGLDDIHRAWRTFVLVRAQDP 702
QY 693 TPRMYFVADVTGAYDAIPQKLVVVANMIRHSESTYCIROYAVVRDSDSQOVHKSFR 752
DB 703 PPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRYAVVQKAAHGHRKAPKS 761
QY 753 QVTTLSLQPYMGQFLKHLQSDASALRNSVUIEOSISNMSSSSLSLFDPLHPLRHSVVK 812
DB 762 HVSTLTDLQPMRQVVAHLQET--SPLKDAVVIEQSSLSNEASSGLFDVFLRMCCHAVR 819
QY 813 IGDRCYTCQOGIPQSSSLTLLCSLCFGDMENKLPARYORDGLLRFVDDFLVLPPLDQ 872
DB 820 IRGKSYVQCQGIPOGSIILTLCSLCYGDMMENKLPAGIRRDGLLRLVDDFLVLPPLTH 879
QY 873 AKTFILSTLVHGVPEVGMINLOKTVVNPFPBPTLGGAPYQLPAHCLFPWCGLLLDTQT 932
DB 880 AKTFILSTLVHGVPEVGMINLOKTVVNPFPBPTLGGAPYQLPAHCLFPWCGLLLDTQT 939
QY 933 LEVPCDYSYQATSIKTSLSLTSQSVPKACKTWRNKLSSVLRLKCHGLFLDLQVNSLTQVCI 992
DB 940 LEVQSDYSYARTSIRASLTFRNGPKAGNRMRKLFGVLRKCHSLFLDLQVNSLTQVCT 999
QY 993 NIYKIFLLQAYRFHACVQLPFDQVRVRKNLTFPLGIISSQASCCYAILKVNKPMGMLKAS 1052
DB 1000 NIYKILLQAYRFHACVQLPFDQVRVRKNLTFPLGIISSQASCCYAILKVNKPMGMLKAS 1059
QY 1053 GS---FPPEAAHWLCYQAPFLKLAHSAHVIYKCLLGPLRTAOKLCKRKLPEATMTILKAA 1109
DB 1060 GAAGPLPSEAVQWLCHQAPFLKLTTHRVVTVYVPLLSRLRTAOTLSRKLPGTTLTALEAAA 1119
QY 1110 DPALSTDFTILD 1122
DB 1120 NPALPSDFKTLID 1132
RESULT 14
AAG64329
ID AAG64329 standard; protein; 1132 AA.
XX AAG64329;
XX AC
XX 24-SEP-2001 (first entry)
XX Human protein #2.
DE Angiogenesis; cardiact; cell differentiating agent; bone marrow;
KW heart muscle cell; heart disease; human.
XX Homo sapiens.
XX WO200148149-A1.
XX 05-JUL-2001.
XX 28-FEB-2000; 2000WO-JP001148.
XX 28-DEC-1999; 99JP-00372826.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K;
XX WPI; 2001-418252/44.
DR N-PSDB; AAH49601.

XX New adult bone marrow-originated cells capable of differentiating into
PT heart muscle cells, applicable as remedies for various heart diseases
PT particularly with damaged heart muscle accompanying degeneration.
XX
PS Disclosure; Page 128-134; 158pp; Japanese.
XX
XX The present invention relates to cells isolated from bone marrow, which
CC are capable of at least differentiating into heart muscle cells. The
CC cells are applicable as remedies for various heart diseases particularly
CC with damaged heart muscle accompanying degeneration. The present sequence
CC was used to illustrate the present invention
XX
SQ Sequence 1132 AA;

Query Match 59.4%; Score 3505; DB 4; Length 1132;
Best Local Similarity 62.4%; Pred. No. 0;
Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;
Qy 1 MTRAPRCAPVRLSRLSRYEVWPLATFVRRILGPGRRILVQPGDKIVRTLVAQCILCMHW 60
Db 1 MPRAPRCARVRLSRLSRYEVWPLATFVRRILGPGRRILVQPGDKIVRTLVAQCILCMHW 60
Qy 61 GSQPPADLSFHQVSSSLKELVARVQRLCERNERNVLAFFGELLNEARFGPPMAFTSSVR 120
Db 61 DARPPAPAPSPQVSCLEKELVARVQRLCERNERNVLAFFGELLNEARFGPPMAFTSSVR 120
Qy 121 SYLNTVJETIRVSGAMWLLSRVGGDDLLVLLAHALCALYLLVPSCAYQVCGSPYQICA 180
Db 121 SYLNTVJETIRVSGAMWLLSRVGGDDLLVLLAHALCALYLLVPSCAYQVCGSPYQICA 180
Qy 181 TTDIWPVSASVYRTPRGVFTNLRLFLQIKSSSRQEAPEKPLALPSRGTKRHLSTSTS 240
Db 181 ATQARPPPHAS-GRRRUG-----CERAWNSVREAGVPLGLPAPGARRGGSASRS 231
Qy 241 VPSAKKARCYVPVVEEGP-----HRQVLFTSGKSW-VPSPARSPVEPTABKLSKK 292
Db 241 VPSAKKARCYVPVVEEGP-----HRQVLFTSGKSW-VPSPARSPVEPTABKLSKK 292
Qy 232 LPLPKRPRGAAPERPFPVQGSWAHPGRTRGSDRGFCVSPAR-----PABEATSL 286
Db 232 LPLPKRPRGAAPERPFPVQGSWAHPGRTRGSDRGFCVSPAR-----PABEATSL 286
Qy 293 GKVSLSLS-GSVCKKHPSSTLSPPQNAQLRP-FIETRIPLYSRGQGRNLNPSF 350
Db 293 GKVSLSLS-GSVCKKHPSSTLSPPQNAQLRP-FIETRIPLYSRGQGRNLNPSF 350
Qy 287 GALSCTRHSFSGVGRHAGPSTSRPPRWDTPCPVYAEYKHFYSSGD-KEQLRPSF 345
Db 287 GALSCTRHSFSGVGRHAGPSTSRPPRWDTPCPVYAEYKHFYSSGD-KEQLRPSF 345
Qy 351 LLSNLQPNLTGARRIVEIIFLGSRPRTSGPLCRTHLSRRYQWMPPLFOQLLVNHAECY 410
Db 351 LLSNLQPNLTGARRIVEIIFLGSRPRTSGPLCRTHLSRRYQWMPPLFOQLLVNHAECY 410
Qy 346 LLSLRPSLTGARRIVEIIFLGSRPRTSGPLCRTHLSRRYQWMPPLFOQLLVNHAECY 405
Db 346 LLSLRPSLTGARRIVEIIFLGSRPRTSGPLCRTHLSRRYQWMPPLFOQLLVNHAECY 405
Qy 411 VRLLRSHCRFTANQOQVTDAL-----NTSPHMLDLRLHSSPMQVY 452
Db 411 VRLLRSHCRFTANQOQVTDAL-----NTSPHMLDLRLHSSPMQVY 452
Qy 406 GVLLKTHCPRLAA---VTPAAGVCAREKPGQSVAAPEBEDTDRRLVQLLRHSSPMQVY 462
Db 406 GVLLKTHCPRLAA---VTPAAGVCAREKPGQSVAAPEBEDTDRRLVQLLRHSSPMQVY 462
Qy 453 GFLRACLCKVYSASLWGRTHRRERPPKULKFIKSLGKYGKLSLOELMWKMKVEDCHWLS 512
Db 453 GFLRACLCKVYSASLWGRTHRRERPPKULKFIKSLGKYGKLSLOELMWKMKVEDCHWLS 512
Qy 463 GFVRACLRLVPPGLMGSRHRRERFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLR 522
Db 463 GFVRACLRLVPPGLMGSRHRRERFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLR 522
Qy 513 SPKDRVPAAEHRLRERILATFLWMDTVVOLLRSFFYITESTFOKNRPFYFRKSVWS 572
Db 513 SPKDRVPAAEHRLRERILATFLWMDTVVOLLRSFFYITESTFOKNRPFYFRKSVWS 572
Qy 523 SPGVGCVPAAEHRLRERILATFLWMDTVVOLLRSFFYITESTFOKNRPFYFRKSVWS 582
Db 523 SPGVGCVPAAEHRLRERILATFLWMDTVVOLLRSFFYITESTFOKNRPFYFRKSVWS 582
Qy 573 KLSQIGVRQHLRVLRLSRLSRLSRYEVWPLATFVRRILGPGRRILVQPGDKIVRTLVAQCILCMHW 632
Db 573 KLSQIGVRQHLRVLRLSRLSRLSRYEVWPLATFVRRILGPGRRILVQPGDKIVRTLVAQCILCMHW 632
Qy 593 KLSQIGVRQHLRVLRLSRLSRLSRYEVWPLATFVRRILGPGRRILVQPGDKIVRTLVAQCILCMHW 642
Db 593 KLSQIGVRQHLRVLRLSRLSRLSRYEVWPLATFVRRILGPGRRILVQPGDKIVRTLVAQCILCMHW 642
Qy 633 RALGRKQAQHTQRLKTLFMSMLYERTKHPHLMGSSVLGNDIYRTWRVFLRVLRALDQ 692
Db 633 RALGRKQAQHTQRLKTLFMSMLYERTKHPHLMGSSVLGNDIYRTWRVFLRVLRALDQ 692
Qy 643 RTFREKRAERLTSRKALFSLVNERARRPCLLGASVLGLDDIHRAWRTTVLRQAQP 702
Db 643 RTFREKRAERLTSRKALFSLVNERARRPCLLGASVLGLDDIHRAWRTTVLRQAQP 702
Qy 693 TPRMYFVKADVTGADATPOGKLVENVANMRHSESTYCIROYAVVRDSOGVHKSPRR 752
Db 693 TPRMYFVKADVTGADATPOGKLVENVANMRHSESTYCIROYAVVRDSOGVHKSPRR 752
Qy 703 PPFLYFVKVDVTGADATPOGKLVENVANMRHSESTYCIROYAVVRDSOGVHKSPRR 761
Db 703 PPFLYFVKVDVTGADATPOGKLVENVANMRHSESTYCIROYAVVRDSOGVHKSPRR 761
Qy 753 QVTTLSDLQPYMGOPKLHQLSDASALRNSVVIEQISIMNSSSSSLFFFLHFLRHSYVK 812
Db 753 QVTTLSDLQPYMGOPKLHQLSDASALRNSVVIEQISIMNSSSSSLFFFLHFLRHSYVK 812

Db 762 HVSTLTDLQPMRQFVAHQET--SPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVR 819
Qy 813 IGRCYTCOCGIGPOGSSLSLLCSLCFQDMENKLFQVQDRDGLLLRFVDDFLVTPHLDQ 872
Db 820 IRGKSYVQCGIGPOGSSLSLLCSLCFQDMENKLFQVQDRDGLLLRFVDDFLVTPHLDQ 879
Qy 873 AKTFSLTLVHGVPEYGCWMLNQLQTVVNPFPVPGTGLGAAPYQLPAHCLFPMCGLLLDQT 932
Db 880 AKTFSLTLVHGVPEYGCWMLNQLQTVVNPFPVPGTGLGAAPYQLPAHCLFPMCGLLLDQT 939
Qy 933 LEVFCDSYGAQTSIKTSLTFQSVFQKAGTWRNKLKSLVRLKCHGLFLDLQVNSLQTVCI 992
Db 940 LEVQSDYSYARTSIRASLTFRNGFKAGRNRRKLFGLVRLKCHSLFLDLQVNSLQTVCT 999
Qy 993 NIYKIFLLQAYRFHACVQLPFDQVRKNTLTFGLIISSOASCCYAILKVNKPMGLKAS 1052
Db 1000 NIYKIFLLQAYRFHACVQLPFDQVRKNTLTFGLIISSOASCCYAILKVNKPMGLKAS 1059
Qy 1053 GS---FPPEAAHMLCYQAFLLKLAHSAVYIKLLGRLTAQKLCRKLPEATMTILKAAA 1109
Db 1060 GAAGPLPSEAVQMLCHQAFLLKLAHSAVYIKLLGRLTAQKLCRKLPEATMTILKAAA 1119
Qy 1110 DPALSTDFQTILD 1122
Db 1120 NPALPSDFKTILD 1132
RESULT 15
AAB99930
ID AAB99930 standard; protein; 1132 AA.
XX AAB99930;
XX AC AAB99930;
XX AC AAB99930;
XX DT 26-SEP-2001 (first entry)
XX Human telomerase protein sequence SEQ ID NO:31.
XX DE Differentiation; heart muscle cell; cytokine; transcription factor;
XX KW proliferation; surface antigen; heart disease; cardiomyocyte;
XX KW bone marrow; umbilical blood cell; heart muscle degeneration;
XX KW myocardial infarction.
XX OS Homo sapiens.
XX OS WO200148150-A1.
XX PN 05-JUL-2001.
XX PD 02-NOV-2000; 2000WO-JP007741.
XX PF 28-DEC-1999; 99JP-00372826.
XX PR 28-FEB-2000; 2000WO-JP001148.
XX XX (KYOW) KYOWA HAKKO KOGYO KK.
XX XX Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
XX XX Yamada Y;
XX XX WPI; 2001-425655/45.
XX XX N-PSDB; AAH44366.
XX DR Cells capable of differentiating into cardiomyocytes and originating in
XX DR bone marrow or umbilical blood cells for study of cardiomyocyte
XX PT differentiation and treatment of heart disease.
XX PT Claim 146; Page 137-141; 187pp; Japanese.
XX CC The present invention describes cells originating in bone marrow or
XX CC umbilical blood cells which are capable of differentiating into
XX CC cardiomyocytes. Also described are: (1) cardiomyocytes produced by the
XX CC differentiation of the cells; (2) a method for carrying out the
XX CC differentiation into cardiomyocytes, regulated by a promotional and/or
XX CC inhibitory factor; (3) a method for the differentiation of the cells into

cell types other than cardiomyocytes; (4) drug compositions promoting the formation of heart muscle and regeneration of heart tissue which contain the cells; (5) a method for the production of antibodies which recognise the cells; (6) a method for screening factors which recognise a surface antigen on the cells; (7) a method for screening factors which promote the proliferation of the cells; (8) a method for immortalising the cells by expressing telomerase in them; (9) drug compositions for the treatment of heart disease which contain the immortalised cells; and (10) cell-free supernatant from the culture of the cells and its use in promoting their differentiation into cardiomyocytes. The cells are used in the treatment of diseases involving heart muscle degeneration, such as myocardial infarction and in the study of cardiomyocyte differentiation. AA44351 to AA44409 and AA44409 to AA444351 represent sequences used in the exemplification of the present invention

Sequence 1132 AA;

Query Match 59.4%; Score 3505; DB 4; Length 1132;
Best Local Similarity 62.4%; Pred. No. 0;
Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;

QY 1 MTRAPRCAPVRSLLSRVEMVPLATFVRRLGPEGRLVQPGDPKIRYRLVAQCLVCMHW 60
DB 1 MPRAPRCAPVRSLLSRVEMVPLATFVRRLGPEGRLVQPGDPKIRYRLVAQCLVCMHW 60

QY 61 GSQPPADLSFHQVSSKELVARVQRLCERNERNVLAFFGPELLNEARGGPPMAFTSSVR 120
DB 61 DARPPAPAPSPQVSKELVARVQRLCERNERNVLAFFGPELLNEARGGPPMAFTSSVR 120

QY 121 SYLNTVITLAVSGAMLLSRVGDLLVYLAHLCALVLLVPPSCAYQVCSPLVYQCA 180
DB 121 SYLNTVITLAVSGAMLLSRVGDLLVYLAHLCALVLLVPPSCAYQVCSPLVYQCA 180

QY 181 TTDIVPSVSAYRTPRPGNRTNLRFLQIKSSSRQEAPEKPLALPSRGTKEHLSITSTS 240
DB 181 TTDIVPSVSAYRTPRPGNRTNLRFLQIKSSSRQEAPEKPLALPSRGTKEHLSITSTS 240

QY 241 VPSAKKARCPYPRVEEGP-----HRQVLTPTSGKSW-VPSPARSPVPTAEKDLSSK 292
DB 241 VPSAKKARCPYPRVEEGP-----HRQVLTPTSGKSW-VPSPARSPVPTAEKDLSSK 292

QY 293 GKVSLSLS-GVCKCHKPSSTLSLPPRONAFQLRP-FIETRHFLYSRGDQERLNPSF 350
DB 293 GKVSLSLS-GVCKCHKPSSTLSLPPRONAFQLRP-FIETRHFLYSRGDQERLNPSF 350

QY 351 LLSNLQPNLTGARRLVEIIFLGRSPTSGPLCRTHLSRYWOMRPLFOQLLVNHAECOY 410
DB 351 LLSNLQPNLTGARRLVEIIFLGRSPTSGPLCRTHLSRYWOMRPLFOQLLVNHAECOY 410

QY 411 VLLRSHCRFTANQOVTDAL-----NTSPPHLMDLLRLHSSPWQVY 452
DB 411 VLLRSHCRFTANQOVTDAL-----NTSPPHLMDLLRLHSSPWQVY 452

QY 453 GFLRACLCKVVSASLWGTTHNRRFPKNIKKFISLKGKLSLOELMMWKVEDCHWLS 512
DB 453 GFLRACLCKVVSASLWGTTHNRRFPKNIKKFISLKGKLSLOELMMWKVEDCHWLS 512

QY 513 SPKDRVPAEHLRIERILATFLWMDTVVQLLRSPEVITESTFOKRLFFYKSVMS 572
DB 513 SPKDRVPAEHLRIERILATFLWMDTVVQLLRSPEVITESTFOKRLFFYKSVMS 572

QY 573 KLSIGVROHLRRLRELSQEVRRHODTWLAMPICRLRFIPKPNGLRPIVNMYSMGT 632
DB 573 KLSIGVROHLRRLRELSQEVRRHODTWLAMPICRLRFIPKPNGLRPIVNMYSMGT 632

QY 633 RALGRKQOAHFTQRLKTLFSLMNTYRTHKPHLMSSVLGMDIYRTWPAFVLRVRLDQ 692
DB 633 RALGRKQOAHFTQRLKTLFSLMNTYRTHKPHLMSSVLGMDIYRTWPAFVLRVRLDQ 692

QY 693 TPRMYFVKADVTGADAIPOGKLVEVVMIRHSSTYCIROYAVVRDSQGVHKSFR 752
DB 693 TPRMYFVKADVTGADAIPOGKLVEVVMIRHSSTYCIROYAVVRDSQGVHKSFR 752

QY 752 PPELYFVKVDVTGADVTIPQDLTEVIASIIK-PQNTYCVRRYAVVQKAAHGHVRKAFKS 761
DB 752 PPELYFVKVDVTGADVTIPQDLTEVIASIIK-PQNTYCVRRYAVVQKAAHGHVRKAFKS 761

QY 753 QVTLSDLPYMGQFLKHLQSDASALRNSVUIEQSISWNESSSLPDPFLPLRHSVVK 812
DB 753 QVTLSDLPYMGQFLKHLQSDASALRNSVUIEQSISWNESSSLPDPFLPLRHSVVK 812

QY 812 HVSTLTDLPYMRQFVAHLOET--SPLRDVUIEQSSLSNEASSGLFDVFLRPMCHAVR 819
DB 812 HVSTLTDLPYMRQFVAHLOET--SPLRDVUIEQSSLSNEASSGLFDVFLRPMCHAVR 819

QY 819 IGDRCYTCOCQIPQSSSLTLLCSLCFGDMENKLPABVQORDGLLRFFVDDFLVTPHLDQ 872
DB 819 IGDRCYTCOCQIPQSSSLTLLCSLCFGDMENKLPABVQORDGLLRFFVDDFLVTPHLDQ 872

QY 872 IRGKSYVOCQIPQSSSLTLLCSLCYGDENKLPAGIRRDGLLRLLVDDFLVTPHLDQ 879
DB 872 IRGKSYVOCQIPQSSSLTLLCSLCYGDENKLPAGIRRDGLLRLLVDDFLVTPHLDQ 879

QY 879 AKTFLSTLVHGVPEYGCMMINIQTVMVPPVBPFTLGGAAAPYQLPAHCLFPWCGLLDQ 932
DB 879 AKTFLSTLVHGVPEYGCMMINIQTVMVPPVBPFTLGGAAAPYQLPAHCLFPWCGLLDQ 932

QY 932 AKTFLSTLVHGVPEYGCMMINIQTVMVPPVBPFTLGGAAAPYQLPAHCLFPWCGLLDQ 939
DB 932 AKTFLSTLVHGVPEYGCMMINIQTVMVPPVBPFTLGGAAAPYQLPAHCLFPWCGLLDQ 939

QY 939 LEVPCDYSYQAQTSIKTSITQSVFKAGKTWRNKLVLRLKCHGLPLDLQVNSLOTVCI 992
DB 939 LEVPCDYSYQAQTSIKTSITQSVFKAGKTWRNKLVLRLKCHGLPLDLQVNSLOTVCI 992

QY 992 LEVQSDYSYARTSIRASLTFRNPGFAGNRKRKLFGVLRKCHSLFLDLQVNSLOTVCT 999
DB 992 LEVQSDYSYARTSIRASLTFRNPGFAGNRKRKLFGVLRKCHSLFLDLQVNSLOTVCT 999

QY 999 NIYKIFLQAYRFHACVIOQLPDDQVRKLNLTFFLGIISQASCCYAILKVNKPMGMLKAS 1052
DB 999 NIYKIFLQAYRFHACVIOQLPDDQVRKLNLTFFLGIISQASCCYAILKVNKPMGMLKAS 1052

QY 1052 NIYKIFLQAYRFHACVIOQLPDDQVRKLNLTFFLGIISQASCCYAILKVNKPMGMLKAS 1059
DB 1052 NIYKIFLQAYRFHACVIOQLPDDQVRKLNLTFFLGIISQASCCYAILKVNKPMGMLKAS 1059

QY 1059 GS---PPPEAAHWLCYQAFLLKLAHSAHSVIYKCLLGLPLTAQKLLCRKLPEATMTILKAA 1109
DB 1059 GS---PPPEAAHWLCYQAFLLKLAHSAHSVIYKCLLGLPLTAQKLLCRKLPEATMTILKAA 1109

QY 1109 GAAGPLPSEAVQWLCHQAFLLKLTERRVTVVPLGLSLRTAQQLSRKLPGLTTLTALEAAA 1119
DB 1109 GAAGPLPSEAVQWLCHQAFLLKLTERRVTVVPLGLSLRTAQQLSRKLPGLTTLTALEAAA 1119

QY 1119 DPALSTDPQTILD 1122
DB 1119 DPALSTDPQTILD 1122

QY 1122 NPALPSDFKTILD 1132
DB 1122 NPALPSDFKTILD 1132

Search completed: May 15, 2006, 13:30:22
Job time : 196 secs

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